

Fri Feb 23 12:03:04 2001

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 22, 2001, 18:19:54 ; Search time 12.32 seconds
(without alignments)
996.084 Million cell updates/sec

US-09-316-080-2
Title: 2050
Sequence: 1 MENPTEFLMTSVLLELYI.....DYDVKELKPLLSIEIYVE 380

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2025.5	98.8	TRIS_GIBPU	P27679 gibberella
2	1966.5	95.9	TRIS_FUSPO	Q00835 fusarium po
3	1961.5	94.7	TRIS_FUSPO	P13513 fusarium sp
4	1899.5	91.2	TRIS_GIBZE	Q00909 gibberella
5	1554	75.8	TRIS_STACH	O59947 stachybotry
6	1525	74.4	TRIS_MYRO	O13489 myrothecium
7	136	6.6	POL_SFW3L	P27401 simian foam
8	101.5	5.0	MYRC_STRCO	Q92512 streptomyc
9	100.5	4.9	SCYL_YEAST	P53009 saccharomyc
10	97.5	4.8	TRNI_SCORI	P76228 escherichia
11	96	4.7	TRNI_SCORI	P46082 clostridium
12	96	4.7	TRNI_SCORI	P18948 caenorhabdi
13	94.5	4.6	PER2_LACLA	P11533 gallus gall
14	94	4.6	CLH_SCHPO	O10161 schizosacch
15	93	4.5	MUTS_AQUUP	P70705 aquilex pyr
16	92.5	4.5	FDEF_YEAST	P29784 saccharomyc
17	92	4.5	PEP3_YEAST	P27801 saccharomyc
18	92	4.5	Y228_BOBBU	O51246 borrelia bu
19	92	4.5	PEPO_LACLA	O07744 lactococcu
20	91.5	4.5	ANG2_YEAST	P03085 saccharomyc
21	91.5	4.5	EVGI_YEAST	P33474 saccharomyc
22	91	4.4	VPA_BPP2	O09145 lactococcu
23	90.5	4.4	PEPO_LACLA	P48996 caenorhabdi
24	90.5	4.4	DP27_CAEEL	O75962 homo sapien
25	90.5	4.4	TRIO_HUMAN	O06666 clostridium
26	90.5	4.4	BKEN_CLOBU	O38677 acetabulari
27	90	4.4	VAAL_ACEAT	O39442 beta vulgar
28	89.5	4.4	VATA_BETUV	P13693 emetiolella
29	89.5	4.4	AMRD_EMENT	P14124 lactococcu
30	89.5	4.4	PER1_LACLA	P24658 canine dist
31	89	4.3	RRPL_CDVO	P13395 drosophila
32	88.5	4.3	SPCA_DROME	
33	88	4.3		

RESULT	1	STANDARD	PRT	383 AA
TRIS_GIBPU				
AC	P27679			
DR	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DE	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	TRICHOIDEENE SYNTHASE (EC 4.1.99.6) (SEQUITERPENE CYCLASE) (TS).			
GN	TRIS OR TOX5.			
OS	Gibberella pulicaris.			
OC	Eukaryota; Fungi; Ascomycota; Hypocreales; Nectriaceae; Gibberella.			
RN	[1]			
RP	SEQUENCE FROM N.A. pubmed-1421511;			
RX	MEDLINE-93043495; Desjardins A.E.;			
RA	Hohn T.M., Desjardins A.E.;			
RT	"Isolation and gene disruption of the Tox5 gene encoding trichodiene synthase in Gibberella pulicaris."			
RI	Mol. Plant Microbe Interact. 5:249-256(1992).			
CC	-1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES. IT CATALYZES THE ISOMERIZATION AND CYLIZATION OF FARNESYL PYROPHOSPHATE TO FORM TRICHOIDEENE, THE FIRST CYCLIC INTERMEDIATE IN THE BIOSYNTHETIC PATHWAY FOR THE ISOPRENOD PATHWAY.			
CC	THE BIOSYNTHETIC PATHWAY FOR TRICHOIDEENES ARE			
CC	TRICHOIDEENE BIOSYNTHESIS. TRICHOIDEENES ARE			
CC	-1- CATALYTIC ACTIVITY: 2-TRANS,6-TRANS-FARNESYL DIPHOSPHATE -			
CC	TRICHOIDEENE + PYROPHOSPHATE.			
CC	-1- PATHWAY: TRICHOIDEENE BIOSYNTHESIS. TRICHOIDEENES ARE			
CC	SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN			
CC	BIOSYNTHESIS.			
CC	-----			
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CC	-----			
DR	EMBL: M64348; AAB02038.1;			
KW	LYASE.			
SQ	SEQUENCE 383 AA; 44958 MW; ABB08F0CB662F6 CRC64;			

Query Match 98.8%; Score 2025.5; DB 1; Length 383;
Best Local Similarity 98.2%; Pred. No. 4e-150; 0; Indels 3; Gaps 1;
Matches 376; Conservative

QY	1	MENPTEFLMTSVLLELYI	RYRDSNYTREERIEMLHYAVKKAHRAPOOOLKAYDP	60
DB	1	MENPTEFLMTSVLLELYI	RYRDSNYTREERIEMLHYAVKKAHRAPOOOLKAYDP	60
QY	61	KRLQSLQIVGVVYVSMANVSKCADLSIHATYIVLVDDSDDPYAMANNYENDLQAG	120	
DB	61	KRLQSLQIVGVVYVSMANVSKCADLSIHATYIVLVDDSDDPYAMANNYENDLQAG	120	
QY	121	REQAHWALVNEHPNVLRFHGFCSLNLIRSTLDFEGCIEQYNGGPGSGHDYPOF	180	
DB	121	REQAHWALVNEHPNVLRFHGFCSLNLIRSTLDFEGCIEQYNGGPGSGHDYPOF	180	

DB 121 RQAHFPMALVNEHPNVLNHFPGCSLNLIRSTLDFEBCGTEIOYNGFGPSHDYPOF 180
 QY 181 LRRNGLGHCVCASLMPKQEDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 DB 181 LRRNGLGHCVCASLMPKQEDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 QY 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKOMAVAFSDKDPVMDTTECFMHCYVWHL 300
 DB 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKOMAVAFSEKDPVMDTTECFMHCYVWHL 300
 QY 301 CDHRRLNEIYEKVGOKTEADQKCFEYQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 359
 DB 301 CDHRRLNEIYEKVGOKTEADQKCFEYQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 359
 QY 360 --KDVAVEIKRPLSLSTEIVE 380
 DB 361 DKAVKDLKEIKRPLSLSTEIVE 383

RESULT 2

TRIS_FUSPO STANDARD; PRT: 377 AA.
 000835;

DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRICHODIENE SYNTHASE (EC 4.1.99.6) (SESQUITERPENE CYCLASE) (TS).
 OS TRIS OR TOX5.
 CC Fusarium poae.
 CC Eukaryota; Fungi; Ascomycota; amorphous Ascomycota; Fusarium.
 RN [1]
 RP MEDLINE-98095652; PubMed-9433809;
 RA Fekete C., Logrieco A., Glacey G., Hornok L.;
 RT "Screening of fungi for the presence of the trichodiene synthase
 RT encoding sequence by hybridization to the tris gene cloned from
 RT Fusarium poae.";
 RL Mycopathologia 138:91-97(1997).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESEYL PYRO-
 CC PHOSPHATE TO FORM TRICHODIENE, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOTECENES. IT SERVES TO BRANCH
 CC TRICHOTECENE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC CATALYTIC ACTIVITY: 2-TRANS, 6-TRANS-FARNESEYL DIPHOSPHATE -
 CC TRICHODIENE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOTECENE BIOSYNTHESIS. TRICHOTECENES ARE
 CC SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 CC BIOSYNTHESIS.

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 CC or send an email to license@isb-sib.ch).
 CC EMBL: U5658; AAA50765.1; -
 CC Lysase.
 DR EMBL: U5658; AAA50765.1; -
 DR Lysase.
 KM Lysase.
 SO SEQUENCE 377 AA; 44157 MW; B483DF3CB730F6AB CRC64;

Query Match 95.9%; Score 1966.5; DB 1; Length 377;
 Best Local Similarity 96.3%; Pred. No. 1.5e-145;
 Matches 366; Conservative 6; Mismatches 5; Indels 3; Gaps 1;

QY 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAOPROOQLKAVDP 60
 DB 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAOPROOQLKAVDP 60
 QY 61 KRLQASLQITVGVVYVSAKSKCEKADLSIRYTYLVLDSSDDPYFAMANYFNDLQAG 120
 DB 61 KRLQASLQITVGVVYVSAKSKCEKADLSIRYTYLVLDSSDDPYFAMANYFNDLQAG 120

QY 121 RQAHFPMALVNEHPNVLNHFPGCSLNLIRSTLDFEBCGTEIOYNGFGPSHDYPOF 180
 DB 121 RQAHFPMALVNEHPNVLNHFPGCSLNLIRSTLDFEBCGTEIOYNGFGPSHDYPOF 180
 QY 181 LRRNGLGHCVCASLMPKQEDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 DB 181 LRRNGLGHCVCASLMPKQEDERGLFLEITSAIQMNNMVMVNDLMSFYKEPDERDQ 240
 QY 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKOMAVAFSDKDPVMDTTECFMHCYVWHL 300
 DB 241 ISLVNRYVVSDEITLHEALEKLTQDTLHSSKOMAVAFSEKDPVMDTTECFMHCYVWHL 300
 QY 301 CDHRRLNEIYEKVGOKTEADQKCFEYQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 360
 DB 301 CDHRRLNEIYEKVGOKTEADQKCFEYQAAVAVGAVSPSEMAVPPVLAOLANIRSKDV 360
 QY 361 DKAVKDLKEIKRPLSLSTEIVE 380
 DB 361 DKAVKDLKEIKRPLSLSTEIVE 383

RESULT 3

TRIS_FUSPO STANDARD; PRT: 374 AA.
 013513;

DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRICHODIENE SYNTHASE (EC 4.1.99.6) (SESQUITERPENE CYCLASE) (TS).
 OS TRIS OR TOX 5.
 CC Fusarium sporotrichoides.
 CC Eukaryota; Fungi; Ascomycota; amorphous Ascomycota; Fusarium.
 RN [1]
 RP MEDLINE-89378769; PubMed-2777086;
 RA Bohn T.M., Beremand P.D.;
 RT "Isolation and nucleotide sequence of a sesquiterpene cyclase gene
 RT from the trichothecene-producing fungus Fusarium sporotrichoides.";
 RL Gene 79:131-138(1989).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESEYL PYRO-
 CC PHOSPHATE TO FORM TRICHODIENE, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOTECENES. IT SERVES TO BRANCH
 CC TRICHOTECENE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC CATALYTIC ACTIVITY: 2-TRANS, 6-TRANS-FARNESEYL DIPHOSPHATE -
 CC TRICHODIENE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOTECENE BIOSYNTHESIS. TRICHOTECENES ARE
 CC SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 CC BIOSYNTHESIS.

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 CC or send an email to license@isb-sib.ch).
 CC EMBL: M27246; M213657.1; -
 CC Lysase.
 DR EMBL: M27246; M213657.1; -
 DR Lysase.
 KM Lysase.
 SO SEQUENCE 374 AA; 43999 MW; 189E8FC1663C3763 CRC64;

Query Match 94.7%; Score 1941; DB 1; Length 374;
 Best Local Similarity 94.2%; Pred. No. 1.4e-143;
 Matches 358; Conservative 10; Mismatches 6; Indels 6; Gaps 1;

QY 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAOPROOQLKAVDP 60
 DB 1 MENPTEFLNTSVRLLEYIRYRDSNTTREERINLHYAVNKAHHAFAOPROOQLKAVDP 60

QY 61 KRLQASLQTIYGVNMYVSWATVSEKCNADISHTYTLVLDDSDPPYAMANTFNDLQAG 120
 DB 61 KRLQASLQTIYGVNMYVSWATVSEKCNADISHTYTLVLDDSDPPYAMANTFNDLQAG 120
 QY 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 DB 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 QY 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 DB 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 QY 181 LRRNNGIGHCYVGSILMPKQEDGELFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 DB 181 LRRNNGIGHCYVGSILMPKQEDGELFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 QY 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 DB 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 QY 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 DB 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 QY 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 DB 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 QY 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 DB 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 QY 361 DVKDYKEIQKPLSSIELVE 380
 DB 361 DVKDYKEIQKPLSSIELVE 380
 QY 357 --KDYKEIQKPLSSIELVE 374
 DB 357 --KDYKEIQKPLSSIELVE 374

RESULT 4
 TRIS_GIBZE STANDARD: PRT: 375 AA.

AC 000909;
 DT 15-DEC-1998 (rel. 37, Created)
 DT 15-DEC-1998 (rel. 37, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last annotation update)
 DE TRICHOIDIENE SYNTHASE (EC 4.1.1.99.6) (SESQUITERPENE CYCLASE) (TS).
 GN Gibberella zeae (Fusarium graminearum).
 OS Eukaryota; Fungi; Ascomycota; Hypocreales; Nectriaceae; Gibberella.
 OC (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN-W-8;
 RC MEDLINE-96172749; PubMed-8589414;
 RA Proctor R.H., Hohn T.M., McCormick S.P.;
 RT "Reduced virulence of Gibberella zeae caused by disruption of a
 trichothecene toxin biosynthetic gene."
 RT trichothecene toxin biosynthetic gene."
 RT Mol. Plant Microbe Interact. 8:593-601(1995).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESEYL PYRO-
 CC PHOSPHATE TO FORM TRICHOIDIENE, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOECENES. IT SERVES TO BRANCH
 CC TRICHOECENE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC TRICHOECENE BIOSYNTHESIS FROM THE ISOPRENOID DIPHOSPHATE -
 CC CATALYTIC ACTIVITY: 2-TRANS,6-TRANS-FARNESEYL DIPHOSPHATE -
 CC TRICHOIDIENE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOECENE BIOSYNTHESIS. TRICHOECENES ARE
 CC SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 CC BIOSYNTHESIS.
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 CC EMBL: 032464; AB072033.1;
 DR Lyase.
 KW SEQUENCE 375 AA; 43942 MW; 2224743B33FE218D CRC64;
 SO

Query Match 91.2%; Score 1869.5; DB 1; Length 375;
 Best Local Similarity 90.8%; Pred. No. 5e-138;
 Matches 345; Conservative 17; Mismatches 13; Indels 5; Gaps 1;

QY 1 MENEPTETPLNTSVRLLEYIRYDSNVTREERIENTLHYAVNKAHHPAQROOQLATYDP 60
 DB 1 MENEPTETPLNTSVRLLEYIRYDSNVTREERIENTLHYAVNKAHHPAQROOQLATYDP 60
 QY 61 KRLQASLQTIYGVNMYVSWATVSEKCNADISHTYTLVLDDSDPPYAMANTFNDLQAG 120
 DB 61 KRLQASLQTIYGVNMYVSWATVSEKCNADISHTYTLVLDDSDPPYAMANTFNDLQAG 120
 QY 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 DB 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 QY 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 DB 121 RQAHFWALVNEHPNVLRFHFGPFCSLNIRSTLDFEGCMTIEQYNGGPGSHDYPQF 180
 QY 181 LRRNNGIGHCYVGSILMPKQEDGELFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 DB 181 LRRNNGIGHCYVGSILMPKQEDGELFLEITSAIAQENMMVWVNDLMSFYKEPDERDQ 240
 QY 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 DB 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 QY 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 DB 241 ISLVKNVYVSDTEITLHEALEKLTQDTLHSSKQAVAFSDPOVMOTIECFMNGYVTHL 300
 QY 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 DB 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 QY 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 DB 301 CDHRRRLNEITEYKQGTEDAKQKCFEYQANAVGAVSPSENAVPPVQALANIRSKDYK 360
 QY 361 DVKDYKEIQKPLSSIELVE 380
 DB 361 DVKDYKEIQKPLSSIELVE 380
 QY 359 ---DVKEAQKPLSSIELVE 375
 DB 359 ---DVKEAQKPLSSIELVE 375

RESULT 5
 TRIS_STACH STANDARD: PRT: 383 AA.

AC 059947;
 DT 15-DEC-1998 (rel. 37, Created)
 DT 15-DEC-1998 (rel. 37, Last sequence update)
 DT 15-DEC-1998 (rel. 37, Last annotation update)
 DE TRICHOIDIENE SYNTHASE (EC 4.1.1.99.6) (SESQUITERPENE CYCLASE) (TS).
 GN Stachybotrys chartarum.
 OS Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Stachybotrys.
 OC (1)
 RN SEQUENCE FROM N.A.
 RP Stratus N.A.; Wong B.;
 RC Submitted (MAR-1998) to the EMBL/Genbank/DBU databases.
 RA -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 CC IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESEYL PYRO-
 CC PHOSPHATE TO FORM TRICHOIDIENE, THE FIRST CYCLIC INTERMEDIATE IN
 CC THE BIOSYNTHETIC PATHWAY FOR TRICHOECENES. IT SERVES TO BRANCH
 CC TRICHOECENE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC -1- CATALYTIC ACTIVITY: 2-TRANS,6-TRANS-FARNESEYL DIPHOSPHATE -
 CC TRICHOIDIENE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOECENE BIOSYNTHESIS. TRICHOECENES ARE
 CC SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 CC BIOSYNTHESIS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: AF053926; M012640.1;
 DR Lyase.
 KW SEQUENCE 383 AA; 44988 MW; F311F432F6E82EDC CRC64;
 SO

Query Match 75.8%; Score 1554; DB 1; Length 383;
 Best Local Similarity 77.5%; Pred. No. 1.6e-113;
 Matches 282; Conservative 33; Mismatches 43; Indels 0; Gaps 0;

DB 1 MEMPTFEFLGAVRLLENVVKIRDSNRYREVENIQAAYNNAAHFQERQOQILKXSP 60
 QY 61 KRLQASLQIYGVAVVYVSNVAKVSEKCNADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 DB 61 KRLASLRTIYGVAVVYVSNVAKVSEKCNADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 QY 121 REQAHPPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEFCGWIQYVNFPGFPGSHDYPOF 180
 DB 121 REQAHPPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEFCGWIQYVNFPGFPGSHDYPOF 180
 QY 181 LRRANGLGHCYASLMPKEQDERGLFLEITSAIOMENMMVNDLSYKFEFDEBQ 240
 DB 181 LRRANGLGHCYASLMPKEQDERGLFLEITSAIOMENMMVNDLSYKFEFDEBQ 240
 QY 241 ISLVKNVYVDEITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDIECFMNGYVTHL 300
 DB 241 ISLVKNVYVDEITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDIECFMNGYVTHL 300
 QY 301 CDHRYRLNLEYEKVKGKTEDAOKCFEYQAAVNGAVSPSEWAPYPIAQLANIRSKDV 360
 DB 301 CDHRYRLNLEYEKVKGKTEDAOKCFEYQAAVNGAVSPSEWAPYPIAQLANIRSKDV 360
 QY 361 DYKD 364
 DB 361 AERD 364

RESULT 6
 ID TRIS MYRO STANDARD: PRT: 385 AA.
 AC 013489:

DB 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE TRICHOIDE NE SYNTHASE (EC 4.1.99.6) (SEQUITERPENE CYCLASE) (TS).
 GN TR15.
 OS Myrothecium rostratum.
 CC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Myrothecium.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN-ATCC 52485;
 RA MEDLINE-98190320; PubMed-9529523;
 RX Trapp S.C., Hohn T.M., McCormick S., Jarvis B.B.;
 RT Characterization of the gene cluster for biosynthesis of macrocyclic
 trichothecenes in Myrothecium rostratum.
 RL Mol. Genet. 257:421-432(1998).
 CC -1- FUNCTION: TS IS A MEMBER OF THE TERPENE CYCLASE GROUP OF ENZYMES.
 IT CATALYZES THE ISOMERIZATION AND CYCLIZATION OF FARNESYL PYRO-
 PHOSPHATE TO FORM TRICHOIDE NE, THE FIRST CYCLIC INTERMEDIATE IN
 THE BIOSYNTHETIC PATHWAY FOR TRICHOIDE NES.
 CC TRICHOIDE NE BIOSYNTHESIS FROM THE ISOPRENOID PATHWAY.
 CC CATALYTIC ACTIVITY: 2-TRANS-6-TRANS-FARNESYL DIPHOSPHATE -
 TRICHOIDE NE + PYROPHOSPHATE.
 CC -1- PATHWAY: TRICHOIDE NE BIOSYNTHESIS. TRICHOIDE NES ARE
 SESQUITERPENOID TOXINS THAT ACT BY INHIBITING PROTEIN
 BIOSYNTHESIS.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: AF009416; AAC49957.1;
 CC Lysase.
 CC DR FM
 CC SEQUENCE 385 AA; 44869 MW; 25A9A2729D5B0D66 CRC64;

Query Match 74.4%; Score 1525; DB 1; Length 385;
 Local Similarity 74.8%; Pred. No. 2.0e-111;

Matches 282; Conservative 37; Mismatches 54; Indels 4; Gaps 1;
 QY 1 MEMPTFEFLGAVRLLENVVKIRDSNRYREVENIQAAYNNAAHFQERQOQILKXSP 60
 DB 1 MEMPTFEFLGAVRLLENVVKIRDSNRYREVENIQAAYNNAAHFQERQOQILKXSP 60
 QY 61 KRLQASLQIYGVAVVYVSNVAKVSEKCNADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 DB 61 KRLASLRTIYGVAVVYVSNVAKVSEKCNADLSIHYYTLVLDDSSDDPYPAMANNFNDLQ 120
 QY 121 REQAHPPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEFCGWIQYVNFPGFPGSHDYPOF 180
 DB 121 REQAHPPMALVNEHPNVLNHFPGFCSLNLIRSTLDFEFCGWIQYVNFPGFPGSHDYPOF 180
 QY 181 LRRANGLGHCYASLMPKEQDERGLFLEITSAIOMENMMVNDLSYKFEFDEBQ 240
 DB 181 LRRANGLGHCYASLMPKEQDERGLFLEITSAIOMENMMVNDLSYKFEFDEBQ 240
 QY 241 ISLVKNVYVDEITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDIECFMNGYVTHL 300
 DB 241 ISLVKNVYVDEITLHEALKEKLTODTLHSSKQAVAFSDKDPQVNDIECFMNGYVTHL 300
 QY 301 CDHRYRLNLEYEKVKGKTEDAOKCFEYQAAVNGAVSPSEWAPYPIAQLANIRSKDV 360
 DB 301 CDHRYRLNLEYEKVKGKTEDAOKCFEYQAAVNGAVSPSEWAPYPIAQLANIRSKDV 360
 QY 361 DYKD 364
 DB 361 AERD 364

RESULT 7
 ID POL SFV3L STANDARD: PRT: 1157 AA.
 AC P27401:

DB 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DE POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE
 TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].
 GN POL.
 OS Simian foamy virus (type 3 / strain LK3) (SFV-3).
 CC Viruses; Retroviridae; Retroviridae; Spumaviridae.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE-92124734; PubMed-1310187;
 RX Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
 RA Neumann-Haefelin D.;
 RT Genomic organization and expression of simian foamy virus type 3
 (SFV-3).
 RL Virology 186:597-608(1992).
 CC -1- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -1- MISCELLANEOUS: THIS POLYPROTEIN IS PROBABLY SYNTHESIZED AS A
 GAG-POL POLYPROTEIN BY A +1 FRAMESHIFT.
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A9.
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CC EMBL: M74895; AAA47796.1;
 CC PIR: B40820; GMLJIK.
 CC HSP: P04385; IRTI.
 CC MEROPS: A09.001;
 CC INTERPRO: IPR000477;
 CC INTERPRO: IPR001037;
 CC INTERPRO: IPR001641;
 CC INTERPRO: IPR002156;
 CC PFM: PF00552; Integrase; 1.